

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANT: Eaton, Dan L.
de Sauvage, Frederic J.

(ii) TITLE OF INVENTION: MPL LIGAND

10 (iii) NUMBER OF SEQUENCES: 21

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Genentech, Inc.
(B) STREET: 460 Point San Bruno Blvd
15 (C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080

20 (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WinPatin (Genentech)

25 (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/430035
(B) FILING DATE: 27-Apr-1995
(C) CLASSIFICATION:

30 (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/196689
(B) FILING DATE: 15-FEB-1994

35 (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/185607
(B) FILING DATE: 21-JAN-1994

40 (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/176553
(B) FILING DATE: 03-JAN-1994

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Winter, Daryl B.
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(C) REFERENCE/DOCKET NUMBER: P0871P2D2

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 415/225-1249
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

10 Leu Leu Leu Val Val Met Leu Leu Leu Thr Ala Arg Leu Thr Leu
-16 -15 -10 -5
Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys
1 5 10
15 Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu
15 20 25 26

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

B' 30 GAATTCCTGG AATACCAGCT GACAATGATT TCCTCCTCAT CTTTCAACCT 50
cont. CACCTCTCCT CATCTAAGAA TTG CTC CTC GTG GTC ATG CTT 91
Leu Leu Leu Val Val Met Leu
-16 -15 -10
35 CTC CTA ACT GCA AGG CTA ACG CTG TCC AGC CCG GCT CCT 130
Leu Leu Thr Ala Arg Leu Thr Leu Ser Ser Pro Ala Pro
-5 1
40 CCT GCT TGT GAC CTC CGA GTC CTC AGT AAA CTG CTT CGT 169
Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu Arg
5 10 15
45 GAC TCC CAT GTC CTT CAC AGC AGA CTG GTGA GAACTCCCAA 210
Asp Ser His Val Leu His Ser Arg Leu
20 25 26
CATTATCCCC TTTATCCGCG TAACTGGTAA GACACCCATA CTCCCAGGAA 260
50 GACACCATCA CTTCTCTAA CTCCTTGACC CAATGACTAT TCTTCCCATA 310
TTGTCCCCAC CTA CTGATCA CACTCTCTGA CAAGAATTAT TCTTCACAAT 360

ACAGCCCGCA TTTAAAAGCT CTCGTCTAGA 390

(2) INFORMATION FOR SEQ ID NO:3:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 390 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

15 TCTAGACGAG AGCTTTTAAA TGCGGGCTGT ATTGTGAAGA ATAATTCTTG 50
TCAGAGAGTG TGATCAGTAG GTGGGGACAA TATGGGAAGA ATAGTCATTG 100
GGTCAAGGAG TTAGAGGAAG TGATGGTGTC TTCCTGGGAG TATGGGTGTC 150
20 TTACCAGTTA CGCGGATAAA GGGGATAATG TTGGGAGTTC TCACCAGTCT 200
GCTGTGAAGG ACATGGGAGT CACGAAGCAG TTTACTGAGG ACTCGGAGGT 250
CACAAGCAGG AGGAGCCGGG CTGGACAGCG TTAGCCTTGC AGTTAGGAGA 300
25 AGCATGACCA CGAGGAGCAA TTCTTAGATG AGGAGAGGTG AGGTTGAAAG 350
ATGAGGAGGA AATCATTGTC AGCTGGTATT CCAGGAATTC 390

30 (2) INFORMATION FOR SEQ ID NO:4:

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 353 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

40 Met Glu Leu Thr Glu Leu Leu Leu Val Val Met Leu Leu Leu Thr
-21 -20 -15 -10
Ala Arg Leu Thr Leu Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu
-5 1 5
45 Arg Val Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser
10 15 20
Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val
25 30 35
50 Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln
40 45 50

	Met	Glu	Glu	Thr	Lys	Ala	Gln	Asp	Ile	Leu	Gly	Ala	Val	Thr	Leu	
	55					60					65					
5	Leu	Leu	Glu	Gly	Val	Met	Ala	Ala	Arg	Gly	Gln	Leu	Gly	Pro	Thr	
	70					75					80					
	Cys	Leu	Ser	Ser	Leu	Leu	Gly	Gln	Leu	Ser	Gly	Gln	Val	Arg	Leu	
	85					90					95					
10	Leu	Leu	Gly	Ala	Leu	Gln	Ser	Leu	Leu	Gly	Thr	Gln	Leu	Pro	Pro	
	100					105					110					
	Gln	Gly	Arg	Thr	Thr	Ala	His	Lys	Asp	Pro	Asn	Ala	Ile	Phe	Leu	
	115					120					125					
15	Ser	Phe	Gln	His	Leu	Leu	Arg	Gly	Lys	Val	Arg	Phe	Leu	Met	Leu	
	130					135					140					
	Val	Gly	Gly	Ser	Thr	Leu	Cys	Val	Arg	Arg	Ala	Pro	Pro	Thr	Thr	
20	145					150					155					
	Ala	Val	Pro	Ser	Arg	Thr	Ser	Leu	Val	Leu	Thr	Leu	Asn	Glu	Leu	
	160					165					170					
25	Pro	Asn	Arg	Thr	Ser	Gly	Leu	Leu	Glu	Thr	Asn	Phe	Thr	Ala	Ser	
	175					180					185					
	Ala	Arg	Thr	Thr	Gly	Ser	Gly	Leu	Leu	Lys	Trp	Gln	Gln	Gly	Phe	
	190					195					200					
30	Arg	Ala	Lys	Ile	Pro	Gly	Leu	Leu	Asn	Gln	Thr	Ser	Arg	Ser	Leu	
	205					210					215					
	Asp	Gln	Ile	Pro	Gly	Tyr	Leu	Asn	Arg	Ile	His	Glu	Leu	Leu	Asn	
35	220					225					230					
	Gly	Thr	Arg	Gly	Leu	Phe	Pro	Gly	Pro	Ser	Arg	Arg	Thr	Leu	Gly	
	235					240					245					
40	Ala	Pro	Asp	Ile	Ser	Ser	Gly	Thr	Ser	Asp	Thr	Gly	Ser	Leu	Pro	
	250					255					260					
	Pro	Asn	Leu	Gln	Pro	Gly	Tyr	Ser	Pro	Ser	Pro	Thr	His	Pro	Pro	
	265					270					275					
45	Thr	Gly	Gln	Tyr	Thr	Leu	Phe	Pro	Leu	Pro	Pro	Thr	Leu	Pro	Thr	
	280					285					290					
	Pro	Val	Val	Gln	Leu	His	Pro	Leu	Leu	Pro	Asp	Pro	Ser	Ala	Pro	
50	295					300					305					

Thr Pro Thr Pro Thr Ser Pro Leu Leu Asn Thr Ser Tyr Thr His
310 315 320

5 Ser Gln Asn Leu Ser Gln Glu Gly
325 330 332

(2) INFORMATION FOR SEQ ID NO:5:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1798 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCGTCTTCCT ACCCATCTGC TCCCCAGAGG GCTGCCTGCT GTGCACTTGG 50

20 GTCCTGGAGC CCTTCTCCAC CCGGATAGAT TCCTCACCCCT TGGCCCGCCT 100

TTGCCCCACC CTACTCTGCC CAGAAGTGCA AGAGCCTAAG CCGCCTCCAT 150

25 GGCCCCAGGA AGGATTCAGG GGAGAGGCC CAAACAGGGA GCCACGCCAG 200

CCAGACACCC CGGCCAGA ATG GAG CTG ACT GAA TTG CTC CTC 242
Met Glu Leu Thr Glu Leu Leu Leu
-21 -20 -15

30 GTG GTC ATG CTT CTC CTA ACT GCA AGG CTA ACG CTG TCC 281
Val Val Met Leu Leu Leu Thr Ala Arg Leu Thr Leu Ser
-10 -5

35 AGC CCG GCT CCT CCT GCT TGT GAC CTC CGA GTC CTC AGT 320
Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser
1 5 10

40 AAA CTG CTT CGT GAC TCC CAT GTC CTT CAC AGC AGA CTG 359
Lys Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu
15 20 25

AGC CAG TGC CCA GAG GTT CAC CCT TTG CCT ACA CCT GTC 398
Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val
30 35

45 CTG CTG CCT GCT GTG GAC TTT AGC TTG GGA GAA TGG AAA 437
Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys
40 45 50

50 ACC CAG ATG GAG GAG ACC AAG GCA CAG GAC ATT CTG GGA 476
Thr Gln Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly
55 60 65

GCA GTG ACC CTT CTG CTG GAG GGA GTG ATG GCA GCA CGG 515
 Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg
 70 75

5 GGA CAA CTG GGA CCC ACT TGC CTC TCA TCC CTC CTG GGG 554
 Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly
 80 85 90

10 CAG CTT TCT GGA CAG GTC CGT CTC CTC CTT GGG GCC CTG 593
 Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu
 95 100

15 CAG AGC CTC CTT GGA ACC CAG CTT CCT CCA CAG GGC AGG 632
 Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg
 105 110 115

20 ACC ACA GCT CAC AAG GAT CCC AAT GCC ATC TTC CTG AGC 671
 Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe Leu Ser
 120 125 130

TTC CAA CAC CTG CTC CGA GGA AAG GTG CGT TTC CTG ATG 710
 Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met
 135 140

25 CTT GTA GGA GGG TCC ACC CTC TGC GTC AGG CGG GCC CCA 749
 Leu Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala Pro
 145 150 155

B' 30 cont. CCC ACC ACA GCT GTC CCC AGC AGA ACC TCT CTA GTC CTC 788
 Pro Thr Thr Ala Val Pro Ser Arg Thr Ser Leu Val Leu
 160 165

35 ACA CTG AAC GAG CTC CCA AAC AGG ACT TCT GGA TTG TTG 827
 Thr Leu Asn Glu Leu Pro Asn Arg Thr Ser Gly Leu Leu
 170 175 180

40 GAG ACA AAC TTC ACT GCC TCA GCC AGA ACT ACT GGC TCT 866
 Glu Thr Asn Phe Thr Ala Ser Ala Arg Thr Thr Gly Ser
 185 190 195

GGG CTT CTG AAG TGG CAG CAG GGA TTC AGA GCC AAG ATT 905
 Gly Leu Leu Lys Trp Gln Gln Gly Phe Arg Ala Lys Ile
 200 205

45 CCT GGT CTG CTG AAC CAA ACC TCC AGG TCC CTG GAC CAA 944
 Pro Gly Leu Leu Asn Gln Thr Ser Arg Ser Leu Asp Gln
 210 215 220

50 ATC CCC GGA TAC CTG AAC AGG ATA CAC GAA CTC TTG AAT 983
 Ile Pro Gly Tyr Leu Asn Arg Ile His Glu Leu Leu Asn
 225 230

GGA ACT CGT GGA CTC TTT CCT GGA CCC TCA CGC AGG ACC 1022
 Gly Thr Arg Gly Leu Phe Pro Gly Pro Ser Arg Arg Thr
 235 240 245

5 CTA GGA GCC CCG GAC ATT TCC TCA GGA ACA TCA GAC ACA 1061
 Leu Gly Ala Pro Asp Ile Ser Ser Gly Thr Ser Asp Thr
 250 255 260

10 GGC TCC CTG CCA CCC AAC CTC CAG CCT GGA TAT TCT CCT 1100
 Gly Ser Leu Pro Pro Asn Leu Gln Pro Gly Tyr Ser Pro
 265 270

15 TCC CCA ACC CAT CCT CCT ACT GGA CAG TAT ACG CTC TTC 1139
 Ser Pro Thr His Pro Pro Thr Gly Gln Tyr Thr Leu Phe
 275 280 285

20 CCT CTT CCA CCC ACC TTG CCC ACC CCT GTG GTC CAG CTC 1178
 Pro Leu Pro Pro Thr Leu Pro Thr Pro Val Val Gln Leu
 290 295

CAC CCC CTG CTT CCT GAC CCT TCT GCT CCA ACG CCC ACC 1217
 His Pro Leu Leu Pro Asp Pro Ser Ala Pro Thr Pro Thr
 300 305 310

25 CCT ACC AGC CCT CTT CTA AAC ACA TCC TAC ACC CAC TCC 1256
 Pro Thr Ser Pro Leu Leu Asn Thr Ser Tyr Thr His Ser
 315 320 325

B' 30
cont. CAG AAT CTG TCT CAG GAA GGG TAA GGTTCCTCAGA CACTGCCGAC 1300
 Gln Asn Leu Ser Gln Glu Gly
 330 332

ATCAGCATTG TCTCATGTAC AGCTCCCTTC CCTGCAGGGC GCCCCTGGGA 1350

35 GACAACTGGA CAAGATTTCC TACTTTCTCC TGAAACCCAA AGCCCTGGTA 1400

AAAGGGATAC ACAGGACTGA AAAGGGAATC ATTTTTCACCT GTACATTATA 1450

40 AACCTTCAGA AGCTATTTTTT TTAAGCTATC AGCAATACTC ATCAGAGCAG 1500

CTAGCTCTTT GGTCTATTTTT CTGCAGAAAT TTGCAACTCA CTGATTCTCT 1550

ACATGCTCTT TTTCTGTGAT AACTCTGCAA AGGCCTGGGC TGGCCTGGCA 1600

45 GTTGAACAGA GGGAGAGACT AACCTTGAGT CAGAAAACAG AGAAAGGGTA 1650

ATTTCCTTTG CTTCAAATTC AAGGCCTTCC AACGCCCCCA TCCCCTTTAC 1700

50 TATCATTCTC AGTGGGACTC TGATCCCATTA TTCTTAACAG ATCTTTACTC 1750

TTGAGAAATG AATAAGCTTT CTCTCAGAAA AAAAAAAAAA AAAAAAAAAA 1798

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1798 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTTTTTTTTT TTTTTTTTTT TCTGAGAGAA AGCTTATTCA TTTCTCAAGA 50
GTAAAGATCT GTTAAGAATA TGGGATCAGA GTCCCACTGA GAATGATAGT 100
AAAGGGGATG GGGGCGTTGG AAGGCCTTGA ATTTGAAGCA AAGGAAATTA 150
CCCTTTCTCT GTTTTCTGAC TCAAGGTTAG TCTCTCCCTC TGTTCAACTG 200
CCAGGCCAGC CCAGGCCTTT GCAGAGTTAT CACAGAAAAA GAGCATGTAG 250
AGAATCAGTG AGTTGCAAAT TTCTGCAGAA AATAGACCAA AGAGCTAGCT 300
GCTCTGATGA GTATTGCTGA TAGCTTAAAA AAATAGCTTC TGAAGGTTTA 350
TAATGTACAG TGAAAAATGA TTCCCTTTTC AGTCCTGTGT ATCCCTTTTA 400
CCAGGGCTTT GGGTTTCAGG AGAAAGTAGG AAATCTTGTC CAGTTGTCTC 450
CCAGGGGCGC CCTGCAGGGA AGGGAGCTGT ACATGAGACA ATGCTGATGT 500
CGGCAGTGTC TGAGAACCTT ACCCTTCCTG AGACAGATTC TGGGAGTGGG 550
TGTAGGATGT GTTTAGAAGA GGGCTGGTAG GGGTGGGCGT TGGAGCAGAA 600
GGGTCAGGAA GCAGGGGGTG GAGCTGGACC ACAGGGGTGG GCAAGGTGGG 650
TGGAAGAGGG AAGAGCGTAT ACTGTCCAGT AGGAGGATGG GTTGGGGAAG 700
GAGAATATCC AGGCTGGAGG TTGGGTGGCA GGGAGCCTGT GTCTGATGTT 750
CCTGAGGAAA TGTCCGGGGC TCCTAGGGTC CTGCGTGAGG GTCCAGGAAA 800
GAGTCCACGA GTTCCATTCA AGAGTTCGTG TATCCTGTTC AGGTATCCGG 850
GGATTTGGTC CAGGGACCTG GAGGTTTGGT TCAGCAGACC AGGAATCTTG 900
GCTCTGAATC CCTGCTGCCA CTTCAGAAGC CCAGAGCCAG TAGTTCTGGC 950
TGAGGCAGTG AAGTTTGTCT CCAACAATCC AGAAGTCCTG TTTGGGAGCT 1000
CGTTCAGTGT GAGGACTAGA GAGGTTCTGC TGGGGACAGC TGTGGTGGGT 1050

GGGGCCCCGCC TGACGCAGAG GGTGGACCCT CCTACAAGCA TCAGGAAACG 1100
 CACCTTTCCT CGGAGCAGGT GTTGAAGCT CAGGAAGATG GCATTGGGAT 1150
 5 CCTTGTGAGC TGTGGTCCTG CCCTGTGGAG GAAGCTGGGT TCCAAGGAGG 1200
 CTCTGCAGGG CCCCAAGGAG GAGACGGACC TGTCCAGAAA GCTGCCCCAG 1250
 10 GAGGGATGAG AGGCAAGTGG GTCCCAAGTTG TCCCCGTGCT GCCATCACTC 1300
 CCTCCAGCAG AAGGGTCACT GCTCCCAGAA TGTCTGTGC CTTGGTCTCC 1350
 TCCATCTGGG TTTTCCATTC TCCCAAGCTA AAGTCCACAG CAGGCAGCAG 1400
 15 GACAGGTGTA GGCAAAGGGT GAACCTCTGG GCACTGGCTC AGTCTGCTGT 1450
 GAAGGACATG GGAGTCACGA AGCAGTTTAC TGAGGACTCG GAGGTCACAA 1500
 GCAGGAGGAG CCGGGCTGGA CAGCGTTAGC CTTGCAGTTA GGAGAAGCAT 1550
 20 GACCACGAGG AGCAATTCAG TCAGCTCCAT TCTGGCCGGG GTGTCTGGCT 1600
 GGCGTGGCTC CCTGTTTGGG GCCTCTCCCC TGAATCCTTC CTGGGGCCAT 1650
 25 GGAGGCGGCT TAGGCTCTTG CACTTCTGGG CAGAGTAGGG TGGGGCAAAG 1700
 GCGGGCCAAG GGTGAGGAAT CTATCCGGGT GGAGAAGGGC TCCAGGACCC 1750
 AAGTGCACAG CAGGCAGCCC TCTGGGGAGC AGATGGGTAG GAAGACGC 1798

B' 30
cont.
(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

40 Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser
 1 5 10 15
 Leu Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro
 20 25 30
 45 Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu
 35 40 45
 Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys
 50 50 55 60

Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe
 65 70 75
 5 Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val
 80 85 90
 Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln
 95 100 105
 10 Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu
 110 115 120
 His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu
 125 130 135
 15 Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp
 140 145 150
 20 Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe
 155 160 165
 Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu
 170 175 180
 25 Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg
 185 190 193

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ser Pro Ala Pro Pro Ala Cys Asp Pro Arg Leu Leu Asn Lys Leu
 1 5 10 15
 40 Leu Arg Asp Asp His Val Leu His Gly Arg
 20 25

(2) INFORMATION FOR SEQ ID NO:9:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu
1 5 10 15

Leu Arg Asp Ser His Val Leu His Ser Arg Leu
20 25 26

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ser Pro Ala Pro Pro Ala Cys Asp Pro Arg Leu Leu Asn Lys Leu
1 5 10 15

Leu Arg Asp Asp Xaa Val Leu His Gly Arg Leu
20 25 26

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Ser Pro Ala Pro Pro Ala Xaa Asp Pro Arg Leu Leu Asn Lys Leu
1 5 10 15

Leu Arg Asp Asp His Val Leu His Gly Arg
20 25

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Xaa Pro Ala Pro Pro Ala Xaa Asp Pro Arg Leu Xaa Asn Lys
1 5 10 14

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs

(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GCCGTGAAGG ACGTGGTCGT CACGAAGCAG TTTATTTAGG AGTCG 45

10 (2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs
(B) TYPE: Nucleic Acid
15 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

20

CCNGCNCNC CNGCNTGYGA 20

(2) INFORMATION FOR SEQ ID NO:15:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

B' 30
cont
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

NCCRTGNARN ACRTGRTCRT C 21

35

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 base pairs
40 (B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

45

CCAGCGCCGC CAGCCTGTGA CCCCCGACTC CTAAATAAAC TGCCTCGTGA 50

TGACCACGTT CAGCACGGC 69

50

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCAGCACCTC CGGCATGTGA CCCCCGACTC CTAAATAAAC TGCTTCGTGA 50
CGACCACGTC CATCACGGC 69

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Pro Arg Leu Leu Asn Lys Leu Leu Arg
1 5 9

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CCAGCACCGC CGGCATGTGA CCCCCGACTC CTAAATAAAC TGCTTCGTGA 50
CGATCATGTC TATCACGGT 69

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GCTAGCTCTA GAAATTGCTC CTCGTGGTCA TGCTTCT 37

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CAGTCTGCCG TGAAGGACAT GG 22

B'
wrd.